

# SEQUENCE LISTING

<110> C. Frank Bennett  
Nicholas M. Dean  
Lex M. Cowsert

<120> ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION

<130> RTS-0066

<160> 182

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<223> Antisense Oligonucleotide

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<210> 2

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<212> DNA

<213> Artificial Sequence

<223> Antisense Oligonucleotide

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<210> 3

<211> 4145

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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agccagctgc aagccccaca gtgaagaaca tctgagctca aatccagata agtgacataa 180

gtgacctgct ttgtaaagcc atagag atg gcc tgt cct tgg aaa ttt ctg ttc 233  
Met Ala Cys Pro Trp Lys Phe Leu Phe  
1 5

aag acc aaa ttc cac cag tat gca atg aat ggg gaa aaa gac atc aac 281  
Lys Thr Lys Phe His Gln Tyr Ala Met Asn Gly Glu Lys Asp Ile Asn  
10 15 20 25

aac aat gtg gag aaa gcc ccc tgt gcc acc tcc agt cca gtg aca cag 329

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Asp	Asp	Leu	Gln	Tyr	His	Asn	Leu	Ser	Lys	Gln	Gln	Asn	Glu	Ser	Pro	
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cag	ccc	ctc	gtg	gag	acg	gga	aag	aag	tct	cca	gaa	tct	ctg	gtc	aag	425
Gln	Pro	Leu	Val	Glu	Thr	Gly	Lys	Lys	Ser	Pro	Glu	Ser	Leu	Val	Lys	
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Leu	Asp	Ala	Thr	Pro	Leu	Ser	Ser	Pro	Arg	His	Val	Arg	Ile	Lys	Asn	
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tgg	ggc	agc	ggg	atg	act	ttc	caa	gac	aca	ctt	cac	cat	aag	gcc	aaa	521
Trp	Gly	Ser	Gly	Met	Thr	Phe	Gln	Asp	Thr	Leu	His	His	Lys	Ala	Lys	
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ggg	att	tta	act	tgc	agg	tcc	aaa	tct	tgc	ctg	ggg	tcc	att	atg	act	569
Gly	Ile	Leu	Thr	Cys	Arg	Ser	Lys	Ser	Cys	Leu	Gly	Ser	Ile	Met	Thr	
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Pro	Lys	Ser	Leu	Thr	Arg	Gly	Pro	Arg	Asp	Lys	Pro	Thr	Pro	Pro	Asp	
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Glu	Leu	Leu	Pro	Gln	Ala	Ile	Glu	Phe	Val	Asn	Gln	Tyr	Tyr	Gly	Ser	
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Phe	Lys	Glu	Ala	Lys	Ile	Glu	Glu	His	Leu	Ala	Arg	Val	Glu	Ala	Val	
	155					160					165					
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Thr	Lys	Glu	Ile	Glu	Thr	Thr	Gly	Thr	Tyr	Gln	Leu	Thr	Gly	Asp	Glu	
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ctc	atc	ttc	gcc	acc	aag	cag	gcc	tgg	cgc	aat	gcc	cca	cgc	tgc	att	809
Leu	Ile	Phe	Ala	Thr	Lys	Gln	Ala	Trp	Arg	Asn	Ala	Pro	Arg	Cys	Ile	
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Ser	Thr	Ala	Arg	Glu	Met	Phe	Glu	His	Ile	Cys	Arg	His	Val	Arg	Tyr	
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tcc	acc	aac	aat	ggc	aac	atc	agg	tcg	gcc	atc	acc	gtg	tte	ccc	cag	953
Ser	Thr	Asn	Asn	Gly	Asn	Ile	Arg	Ser	Ala	Ile	Thr	Val	Phe	Pro	Gln	
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Pro Thr Ser Ser Arg Ala Thr Ile Leu Val Glu Leu Ser Cys Glu Asp	
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Gly Gln Gly Leu Asn Tyr Leu Pro Gly Glu His Leu Gly Val Cys Pro	
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Gly Asn Gln Pro Ala Leu Val Gln Gly Ile Leu Glu Arg Val Val Asp	
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Gly Ser Tyr Trp Val Ser Asp Lys Arg Leu Pro Pro Cys Ser Leu Ser	
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cag gcc ctc acc tac tcc ccg gac atc acc aca ccc cca acc cag ctg	2729
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Leu Leu Gln Lys Leu Ala Gln Val Ala Thr Glu Glu Pro Glu Arg Gln	
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agg ctg gag gcc ctg tgc cag ccc tca gag tac agc aag tgg aag ttc	2825
Arg Leu Glu Ala Leu Cys Gln Pro Ser Glu Tyr Ser Lys Trp Lys Phe	
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acc aac agc ccc aca ttc ctg gag gtg cta gag gag ttc ccg tcc ctg	2873
Thr Asn Ser Pro Thr Phe Leu Glu Val Leu Glu Glu Phe Pro Ser Leu	
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Arg Val Ser Ala Gly Phe Leu Leu Ser Gln Leu Pro Ile Leu Lys Pro	
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Arg Phe Tyr Ser Ile Ser Ser Ser Arg Asp His Thr Pro Thr Glu Ile	
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His Leu Thr Val Ala Val Val Thr Tyr His Thr Gly Asp Gly Gln Gly	
925 930 935	
ccc ctg cac cac ggt gtc tgc agc aca tgg ctc aac agc ctg aag ccc	3065
Pro Leu His His Gly Val Cys Ser Thr Trp Leu Asn Ser Leu Lys Pro	
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Gln Asp Pro Val Pro Cys Phe Val Arg Asn Ala Ser Ala Phe His Leu	
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ccc gag gat ccc tcc cat cct tgc atc ctc atc ggg cct ggc aca ggc	3161
Pro Glu Asp Pro Ser His Pro Cys Ile Leu Ile Gly Pro Gly Thr Gly	
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 Ile Val Pro Phe Arg Ser Phe Trp Gln Gln Arg Leu His Asp Ser Gln  
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 His Lys Gly Val Arg Gly Gly Arg Met Thr Leu Val Phe Gly Cys Arg  
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 Arg Pro Asp Glu Asp His Ile Tyr Gln Glu Glu Met Leu Glu Met Ala  
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 Ser Glu Val Leu Arg Val Leu His Lys Glu Pro Gly His Leu Tyr Val  
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 Cys Gly Asp Val Arg Met Ala Arg Asp Val Ala His Thr Leu Lys Gln  
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 1115 1120 1125

gct gta ttt cct tac gag gcg aag aag gac agg gtg gcg gtg cag ccc 3641  
 Ala Val Phe Pro Tyr Glu Ala Lys Lys Asp Arg Val Ala Val Gln Pro  
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 Ser Ser Leu Glu Met Ser Ala Leu  
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<212> DNA  
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<210> 9  
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<223> PCR Probe

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20

<210> 10

<211> 4145

<212> DNA

<213> Mus musculus

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agccagctgc aagccccaca gtgaagaaca tctgagctca aatccagata agtgacataa 180

gtgacctgct ttgtaaagcc atagag atg gcc tgt cct tgg aaa ttt ctg ttc 233

Met Ala Cys Pro Trp Lys Phe Leu Phe  
1 5

aag acc aaa ttc cac cag tat gca atg aat ggg gaa aaa gac atc aac 281

Lys Thr Lys Phe His Gln Tyr Ala Met Asn Gly Glu Lys Asp Ile Asn  
 10 15 20 25

aac aat gtg gag aaa gcc ccc tgt gcc acc tcc agt cca gtg aca cag 329

Asn Asn Val Glu Lys Ala Pro Cys Ala Thr Ser Ser Pro Val Thr Gln  
30 35 40

gat gac ctt cag tat cac aac ctc agc aag cag cag aat gag tcc ccg 377

Asp Asp Leu Gln Tyr His Asn Leu Ser Lys Gln Gln Asn Glu Ser Pro  
45 50 55

cag ccc ctc gtg gag acg gga aag aag tct cca gaa tct ctg gtc aag 425

Gln Pro Leu Val Glu Thr Gly Lys Lys Ser Pro Glu Ser Leu Val Lys  
60 65 70

ctg gat gca acc cca ttg tcc tcc cca cgg cat gtg agg atc aaa aac 473

Leu Asp Ala Thr Pro Leu Ser Ser Pro Arg His Val Arg Ile Lys Asn  
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tgg ggc agc ggg atg act ttc caa gac aca ctt cac cat aag gcc aaa 521

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Pro Lys Ser Leu Thr Arg Gly Pro Arg Asp Lys Pro Thr Pro Pro Asp

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Phe	Lys	Glu	Ala	Lys	Ile	Glu	Glu	His	Leu	Ala	Arg	Val	Glu	Ala	Val	
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ctc	atc	ttc	gcc	acc	aag	cag	gcc	tgg	cgc	aat	gcc	cca	cgc	tgc	att	809
Leu	Ile	Phe	Ala	Thr	Lys	Gln	Ala	Trp	Arg	Asn	Ala	Pro	Arg	Cys	Ile	
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Ser	Thr	Ala	Arg	Glu	Met	Phe	Glu	His	Ile	Cys	Arg	His	Val	Arg	Tyr	
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Arg	Ser	Asp	Gly	Lys	His	Asp	Phe	Arg	Val	Trp	Asn	Ala	Gln	Leu	Ile	
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gcc	aac	gtg	gaa	ttc	act	cag	ctg	tgc	atc	gac	ctg	ggc	tgg	aag	ccc	1097
Ala	Asn	Val	Glu	Phe	Thr	Gln	Leu	Cys	Ile	Asp	Leu	Gly	Trp	Lys	Pro	
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Ala	Met	Glu	His	Pro	Lys	Tyr	Glu	Trp	Phe	Arg	Glu	Leu	Glu	Leu	Lys	
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Trp	Lys	Asp	Gln	Ala	Val	Val	Glu	Ile	Asn	Ile	Ala	Val	Ile	His	Ser		
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Phe	Gln	Lys	Gln	Asn	Val	Thr	Ile	Met	Asp	His	His	Ser	Ala	Ala	Glu		
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tcc	ttc	atg	aag	tac	atg	cag	aat	gaa	tac	cgg	tcc	cgt	ggg	ggc	tgc	1577	
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ccc	gtg	ttt	cac	cag	gag	atg	ctg	aac	tac	gtc	ctg	tcc	cct	ttc	tac	1673	
Pro	Val	Phe	His	Gln	Glu	Met	Leu	Asn	Tyr	Val	Leu	Ser	Pro	Phe	Tyr		
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Tyr	Tyr	Gln	Val	Glu	Ala	Trp	Lys	Thr	His	Val	Trp	Gln	Asp	Glu	Lys		
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cgg	aga	ccc	aag	aga	aga	gag	att	cca	ttg	aaa	gtc	ttg	gtc	aaa	gct	1769	
Arg	Arg	Pro	Lys	Arg	Arg	Glu	Ile	Pro	Leu	Lys	Val	Leu	Val	Lys	Ala		
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gtg	ctc	ttt	gcc	tgt	atg	ctg	atg	cgc	aag	aca	atg	gcg	tcc	cga	gtc	1817	
Val	Leu	Phe	Ala	Cys	Met	Leu	Met	Arg	Lys	Thr	Met	Ala	Ser	Arg	Val		
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Arg	Val	Thr	Ile	Leu	Phe	Ala	Thr	Glu	Thr	Gly	Lys	Ser	Glu	Ala	Leu		
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gcc	tgg	gac	ctg	ggg	gcc	tta	ttc	agc	tgt	gcc	ttc	aac	ccc	aag	gtt	1913	
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Val	Cys	Met	Asp	Lys	Tyr	Arg	Leu	Ser	Cys	Leu	Glu	Glu	Glu	Arg	Leu		
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Leu	Leu	Val	Val	Thr	Ser	Thr	Phe	Gly	Asn	Gly	Asp	Cys	Pro	Gly	Asn		
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Gly Glu Lys Leu Lys Lys Ser Leu Phe Met Leu Lys Glu Leu Asn Asn	
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aaa ttc agg tac gct gtg ttt ggc ctc ggc tcc agc atg tac cct cgg	2105
Lys Phe Arg Tyr Ala Val Phe Gly Leu Gly Ser Ser Met Tyr Pro Arg	
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Gln Ala Leu Thr Tyr Ser Pro Asp Ile Thr Thr Pro Pro Thr Gln Leu	
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acc aac agc ccc aca ttc ctg gag gtg cta gag gag ttc ccg tcc ctg Thr Asn Ser Pro Thr Phe Leu Glu Val Leu Glu Phe Pro Ser Leu 875 880 885	2873
cgg gtg tct gct ggc ttc ctg ctg tcc cag ctc ccc att ctg aag ccc Arg Val Ser Ala Gly Phe Leu Leu Ser Gln Leu Pro Ile Leu Lys Pro 890 895 900 905	2921
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Ser Ser Leu Glu Met Ser Ala Leu	
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54

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102

Trp	Val	Trp	Val	Ser	Leu	Leu	Val	Ala	Ala	Gly	Thr	Val	Gln	Pro	Ser		
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Asp	Ser	Gln	Ser	Val	Cys	Ala	Gly	Thr	Glu	Asn	Lys	Leu	Ser	Ser	Leu		
	25					30					35						
tct	gac	ctg	gaa	cag	cag	tac	cga	gcc	ttg	cgc	aag	tac	tat	gaa	aac	198	
Ser	Asp	Leu	Glu	Gln	Gln	Tyr	Arg	Ala	Leu	Arg	Lys	Tyr	Tyr	Glu	Asn		
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tgt	gag	gtt	gtc	atg	ggc	aac	ctg	gag	ata	acc	agc	att	gag	cac	aac	246	
Cys	Glu	Val	Val	Met	Gly	Asn	Leu	Glu	Ile	Thr	Ser	Ile	Glu	His	Asn		
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cgg	gac	ctc	tcc	ttc	ctg	cgg	tct	gtt	cga	gaa	gtc	aca	ggc	tac	gtg	294	
Arg	Asp	Leu	Ser	Phe	Leu	Arg	Ser	Val	Arg	Glu	Val	Thr	Gly	Tyr	Val		
			75					80						85			
tta	gtg	gct	ctt	aat	cag	ttt	cgt	tac	ctg	cct	ctg	gag	aat	tta	cgc	342	
Leu	Val	Ala	Leu	Asn	Gln	Phe	Arg	Tyr	Leu	Pro	Leu	Glu	Asn	Leu	Arg		
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Ile	Ile	Arg	Gly	Thr	Lys	Leu	Tyr	Glu	Asp	Arg	Tyr	Ala	Leu	Ala	Ile		
	105					110					115						
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Phe	Leu	Asn	Tyr	Arg	Lys	Asp	Gly	Asn	Phe	Gly	Leu	Gln	Glu	Leu	Gly		
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tta	aag	aac	ttg	aca	gaa	atc	cta	aat	ggt	gga	gtc	tat	gta	gac	cag	486	
Leu	Lys	Asn	Leu	Thr	Glu	Ile	Leu	Asn	Gly	Gly	Val	Tyr	Val	Asp	Gln		
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aac	aaa	ttc	ctt	tgt	tat	gca	gac	acc	att	cat	tgg	caa	gat	att	gtt	534	
Asn	Lys	Phe	Leu	Cys	Tyr	Ala	Asp	Thr	Ile	His	Trp	Gln	Asp	Ile	Val		
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cgg	aac	cca	tgg	cct	tcc	aac	ttg	act	ctt	gtg	tca	aca	aat	ggt	agt	582	
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Ser	Gly	Cys	Gly	Arg	Cys	His	Lys	Ser	Cys	Thr	Gly	Arg	Cys	Trp	Gly		
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ccc	aca	gaa	aat	cat	tgc	cag	act	ttg	aca	agg	acg	gtg	tgt	gca	gaa	678	
Pro	Thr	Glu	Asn	His	Cys	Gln	Thr	Leu	Thr	Arg	Thr	Val	Cys	Ala	Glu		
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caa	tgt	gac	ggc	aga	tgc	tac	gga	cct	tac	gtc	agt	gac	tgc	tgc	cat	726	
Gln	Cys	Asp	Gly	Arg	Cys	Tyr	Gly	Pro	Tyr	Val	Ser	Asp	Cys	Cys	His		
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cga	gaa	tgt	gct	gga	ggc	tgc	tca	gga	cct	aag	gac	aca	gac	tgc	ttt	774	
Arg	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Lys	Asp	Thr	Asp	Cys	Phe		
			235					240						245			

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caa acc ttt gtc tac aat cca acc acc ttt caa ctg gag cac aat ttc Gln Thr Phe Val Tyr Asn Pro Thr Thr Phe Gln Leu Glu His Asn Phe 265 270 275	870
aat gca aag tac aca tat gga gca ttc tgt gtc aag aaa tgt cca cat Asn Ala Lys Tyr Thr Tyr Gly Ala Phe Cys Val Lys Lys Cys Pro His 280 285 290 295	918
aac ttt gtg gta gat tcc agt tct tgt gtg cgt gcc tgc cct agt tcc Asn Phe Val Val Asp Ser Ser Ser Cys Val Arg Ala Cys Pro Ser Ser 300 305 310	966
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gac att tgc cca aaa gct tgt gat ggc att ggc aca gga tca ttg atg Asp Ile Cys Pro Lys Ala Cys Asp Gly Ile Gly Thr Gly Ser Leu Met 330 335 340	1062
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Lys Ala Asn Val Glu Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met	
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Val His Glu His Lys Asp Asn Ile Gly Ser Gln Leu Leu Leu Asn Trp	
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Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn	
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His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp	
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Ser Tyr Gln Ser Asp Leu Lys Glu Glu Lys Asp Ile Asn Asn Asn Val
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Asn Val Pro Glu Ser Leu Asp Lys Leu His Val Thr Ser Thr Arg Pro
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Ile Leu Glu Arg Val Val Asp Cys Pro Thr Pro His Gln Thr Val Cys	
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